

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:54 ; Search time 11.5226 Seconds  
(without alignments)  
3287.177 Million cell updates/sec

Title: US-09-836-077-4  
Perfect score: 2120  
Sequence: 1 MTPPPGGAAPSAPRARVLS.....TFQVADSHPEVAQRVEPMGP 394

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	907.5	42.8	653	2 T03102	semaphorin homolog
2	368	17.4	749	2 G01856	semaphorin V - hum
3	363	17.1	771	2 D49423	semaphorin III pre
4	361.5	17.1	748	2 I48744	semaphorin A - mou
5	355.5	16.8	782	2 I48746	semaphorin C - mou
6	350	16.5	772	2 A49069	collapsin - chicke
7	349	16.5	772	2 I48747	semaphorin D - mou
8	341.5	16.1	441	2 S29921	hypothetical prote
9	340.5	16.1	403	2 E42521	A39R protein - vac
10	331.5	15.6	751	2 I48748	semaphorin E - mou
11	329.5	15.5	666	2 I58169	semaphorin III - m
12	327.5	15.4	753	2 G02173	semaphorin III fam
13	314	14.8	834	2 S66498	M-sema F protein p
14	312	14.7	730	2 JH0798	fasciclin IV precu
15	298	14.1	711	2 A49423	semaphorin I precu
16	296.5	14.0	712	2 T27165	hypothetical prote
17	287.5	13.6	760	2 I48745	semaphorin B - mou
18	274.5	12.9	1074	2 JC5928	semaphorin F precu
19	264	12.5	724	2 C49423	semaphorin II prec
20	260	12.3	656	2 B49423	semaphorin I - fru
21	217.5	10.3	295	2 JQ1775	Sall9R protein - v
22	186	8.8	676	2 T33853	hypothetical prote
23	131	6.2	620	2 T30765	hypothetical prote
24	121	5.7	2051	2 T13164	plexin B - fruit f
25	113	5.3	1894	2 JC4980	plexin 1 precursor
26	110.5	5.2	122	2 C72169	A46R protein - var
27	110.5	5.2	122	2 H36852	A43R protein - var
28	110.5	5.2	122	2 T28584	14R protein - vari
29	110.5	5.2	1375	1 JC5148	hepatocyte growth

30	109.5	5.2	1945	2 T13937	plexin A - fruit f
31	102	4.8	142	2 JQ1776	SallR protein - v
32	102	4.8	399	2 T40831	probable guanine n
33	99	4.7	1948	2 B69511	N conserved hypoth
34	98.5	4.6	929	2 T35683	ftsk homolog - Str
35	98.5	4.6	1905	2 I51553	plexin - African c
36	98	4.6	407	2 H69064	serine/threonine p
37	97	4.6	987	2 D97029	ribonucleotide red
38	97	4.6	1884	2 JC4975	plexin 2 precursor
39	97	4.6	4351	2 T00252	MEGF1 protein - ra
40	96.5	4.6	1272	2 F97568	hypothetical prote
41	96.5	4.6	1272	2 AF2789	hypothetical prote
42	95	4.5	528	2 S32431	abrin-d precursor
43	94.5	4.5	528	1 TZLSA	abrin-a precursor
44	94.5	4.5	903	2 E88221	protein T01H3.2 [1
45	93	4.4	518	2 T23120	hypothetical prote

ALIGNMENTS

RESULT 1

T03102  
semaphorin homolog A3 - alcelaphine herpesvirus 1  
C:Species: alcelaphine herpesvirus 1  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
C:Accession: T03102  
R:Ensser, A.; Pflanz, R.; Fleckenstein, B.  
J. Virol. 71, 6517-6525, 1997  
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.  
A:Reference number: Z14840; MUID:97404659; PMID:9261371  
A:Accession: T03102  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-653 <ENS>  
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58054.1; PID:g2337970

Query Match 42.8%; Score 907.5; DB 2; Length 653;  
Best Local Similarity 48.9%; Pred. No. 1.7e-68;  
Matches 182; Conservative 54; Mismatches 129; Indels 7; Gaps 5;

QY	22	PARFG-LPLRLLLVFWAAASAGHSRSGPRISAVWK---QGDHVDQSQPEPHVLFH	77
DB	45	PRAMGTLCSVIRLLML-SAITAKSRFDKPLIYNLTDFGQ-QHFFGQPEPHVLFH	102
QY	78	EPGSFVWVGGRGVYHFNPECKNASVTVTNGTSGQDQKDCGNYITLLRRNGL	137
DB	103	SLNSSDVYVGGNTIYLFDFAHSSNASTALINITSTHNRHSSTCENFTLLHNQTDGL	162
QY	138	LYCGTNARKPSCHNLVNDVSVSLGEMKGVAPSPDENSILVFEQDEVYSTIRKQEVNGK	197
DB	163	LACGTNSQKPSCH-LNNLTQFLGPKLGLAPSPSGNVLVFDQNDTYSTINLYKSLG	221
QY	198	IPRFRIRGESELYTSDTVNQNPQFIKATIVHQDQYDDKIYFFREDNPKRPEALNV	257
DB	222	SHKFRIGAOVELYSDTAMHRPQVQATAVHKNESYDDKIYFFQENSHSDFKQPHTV	281
QY	258	SRVAQLCRGDQGGESSLSVSKWTFKLKMLVCSDAATNRNFNLDQVFLLPDPSGQWRD	317
DB	282	PRVQGVCSDDQGGESSLSVSKWTFKLKARLACVDYDTGTGRYINELQDIFIWQAPENSWEET	341
QY	318	RYGVFSPNPNYSACVYSLGDDIDRVFTSSLAGYHMLSNRPRGMLPKQIPITETFO	377
DB	342	LIYGLFLSPWNFSACVFTVKVDIDHVFETSKLKNYHKLPTPRPGCMKNHQHVPTETFO	401
QY	378	VADSHPEVAQRV	389
DB	402	VADRYEVAQDPV	413

RESULT 2

G01856  
semaphorin V - human

C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C:Accession: G01856  
R: Sekido, Y.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: G08634  
A:Accession: G01856  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-749 <SEK>  
A:Cross-references: EMBL:U28369, NID:974283; PIDN:AAD09138.1; PID:974284  
C:Superfamily: semaphorin

Query Match 17.1%; Score 368; DB 2; Length 749;  
Best Local Similarity 28.9%; Pred. No. 8.1e-23;  
Matches 127; Conservative 49; Mismatches 167; Indels 96; Gaps 18;

Qy 7 GRAAPSAPRARVLSLPAREGLPLRLRLLLVFWAAASAGHSRSGPRISAVKGGQDHYDF 66  
Db 22 GSAAPSPPLRL-----SFOELQA-WHGLQTESL 49  
Qy 67 SOPEPHTVLFHEPGSFSVWVGKGVYHFNPEGKNASVTVNI-----G 111  
Db 50 ERTCCYQALLVDEERGLFVGAENHVASLNL---DNISKRAKKLAWPAPVWEWEECNWAG 106  
Qy 112 STKGSCQDKQDCGNVITLLER-RGNGLLVCGTNAARKPSC-----WNLVNDVVM-----SL 161  
Db 107 KDIGT-----ECMNFVLLHAYNTHLLACGTGAFHPTCAFEVGHRAEPEVRLDPGR 161  
Qy 162 GEMKGYAPFSPDENSILVFEDEVYSTIRKQYNGKIPFRFRIRGESELYT---SDTVMQ 218  
Db 162 EDGKGKSPYDPRHRAASLVGEELYSVGAADLMGRDFTIFRSLGORPSLRTEPHDSRLN 221  
Qy 219 NPQFIKA-TIVHQDQAYDDKIYFFREDNPKNPE-APLVSRVAQLCRGOGGESSLSV 276  
Db 222 EPKVFVFWPESENPDQDKIYFFRETAVAAPALGRLSVSRVQCICRNDVGGORSL-V 280  
Qy 277 SKWTFKAMLVCS---DAATNRNENRLQDVFLLPDPSCQWRDTRVYGVFSNP---WNYS 331  
Db 281 NKWTFKARLVCSVPGVEGDTDFDQDQVLL---SSRDHRTPLLYAVFSSSIFQCSA 338  
Qy 332 VCIVSLGDIRVF-----RTSSLKGYHMGSLNPRPGMCLPKK-----OPIPT 374  
Db 339 VCIVSMNDVRAFLGLFPFAHKGPMHGWYSYQGRVYPRPGMC-PSKTFGTSTKDFPD 397  
Qy 375 TFQVADSHPEVAQRPEMG 393  
Db 398 VIQFARNHPLMINSVLPNG 416

RESULT 3  
D49423  
semaphorin III precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-Sep-1999  
C:Accession: D49423  
R: Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.  
Cell 75, 1389-1399, 1993  
A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone  
A:Reference number: A49423; MUID:94094332; PMID:8269517  
A:Accession: D49423  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-771 <KOL>  
A:Cross-references: GB:L26081; NID:9799328; PIDN:AAA65938.1; PID:g436560  
C:Genetics:  
A:Gene: GDB:SEMA1  
A:Cross-references: GDB:283448  
C:Superfamily: semaphorin

Query Match 17.1%; Score 363; DB 2; Length 771;  
Best Local Similarity 28.0%; Pred. No. 2.2e-22;  
Matches 119; Conservative 66; Mismatches 162; Indels 78; Gaps 19;

Qy 32 RLLLVFWAAASAGHSRSG-----PRISAVK-----GODHVD-----SOPEPHTVLFHEP 79  
Db 6 RIVCLFWGVLLTARANYONGKNNVPRKLKLSYKEMLESNNVITFNGLANSSVHTFLDDEE 65  
Qy 80 GSFSVWVGKGVYHFNPEGKNASVTVNIGSTKGCQDK-----QDCGNYITLL 130  
Db 66 RS-LUYGAKDHIFFSFDLVNLIKDFQKIVWPVSYTR---RDECKWAGKDILKECANFIKVL 121  
Qy 131 ER-RGNGLLVCGTNARKPSC-----WNLVNDVVMVSLGEMKGYAPFSPDEN 176  
Db 122 KAYNQTHLYACGTGAFHPTCTYIEIGHHPEDNIFKLENS---HFENGKSGSPYDKLLT 177  
Qy 177 LVLEFEGDEVYSTIRKQYNGKIPFRFRIRGESELYT---SDTVMONPOFIKATIVHO-DQ 232  
Db 178 ASLLIDGELYSGTRAADFMRGFAIFRTLCHHHPIHTEOHDNRWLNDRPFISAHLISESDN 237  
Qy 233 AYDKKIYFFREDNPKNPEAPLVSRVAQLCRGOGGESSLSVSKWTFKAMLVCSDA 292  
Db 238 PEDDKVYFFRENADIDGESHGKATHARIGQICKNDFGHRSL-VNKWTFKARLICSVP 296  
Qy 293 ATN---RNENRLQDVFLL---PDPSCQWRDTRVYGVF---SNPNYSACVYSLGDIRVF 344  
Db 297 GPNGIDTHFDELQDVFLLMNFKDP---KNPVYGVYFTTSSNIFKGSAYCMYSMSDVRVF 352  
Qy 345 -----RTSSLKGYHMGSLNPRPGMCLPKK-----OPIPTETFOVADSHPEVAQ 387  
Db 353 LGPVFAHRDGNVQWVYQGRVYPRPGTC-PSKTFEGGDFDNDLPDDVITFARSHPAMYN 411  
Qy 388 RVEPM 392  
Db 412 PVFPM 416

RESULT 4  
I48744  
semaphorin A - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
C:Accession: I48744  
R: Puschel, A.W.; Adams, R.H.; Betz, H.  
Neuron 14, 941-948, 1995  
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat  
A:Reference number: I48744; MUID:95267431; PMID:7748561  
A:Accession: I48744  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-748 <RES>  
A:Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324  
C:Genetics:  
C:Superfamily: semaphorin

Query Match 17.1%; Score 361.5; DB 2; Length 748;  
Best Local Similarity 29.9%; Pred. No. 2.9e-22;  
Matches 133; Conservative 51; Mismatches 152; Indels 109; Gaps 23;

Qy 7 GRAAPSAPRARV---LSLPAREGL-PLRL-----RLLLV-----FWVAAASAQ 45  
Db 22 GDTAPNLPRLRSLFQELQARHGVTFRLETCYCEALLVDEERGLFVGAENHVASLSLD 81  
Qy 46 GHSRSGPRISAVKGGQDHYDFSQPEPHTVLFHEPGSFSVWVGKGVYHFNPEGKNASV 105  
Db 82 NISKRAKLA--W-----PAPVWEWEECN---WAG----- 106  
Qy 106 RTVNIGSTKGCQDKQDCGNVITLLERRGN-GLLVCGTNARKPSC---WNLVNDVVM 160  
Db 107 --KDGT-----ECMNFVLLHAYNTHLLACRTGAFHPTCALWRWATAGGTHAST 155  
Qy 161 ----LGEKMGYAPFSPDENSLVFEDEVYSTIRKQYNGKIPFRFRIRGESELYT---S 213  
Db 156 GPEKLEDKGKGTDPYDPRHPRPSVLVGEELYSVGTADLMGRDFTIFRSLGQNPSLRTEPHD 215

Qy	214	DTVMQNQFIKA-TIVHQDAQYDDKYYFFREDNDPKNPE-APLNVSRVAQLCRGDQGG	271
Db	216	SRWLNEPKFKVKEWIPSESNPDDDKIYFFPRESAVEAAPAMGRMSVSRVGQICRNDLGQ	275
Qy	272	SSLSSVKWNTFLKAMLCVS--DAATNRNFNRLQDVLLPDPSCQWRDT-RVYGVFSNP--	326
Db	276	RSL-VNKKWITFLKARLVCSPVGEVDTHFDQLQDVFL---SSRDQTPLLXAVFSTSSG	331
Qy	327	-WNYSAVVCYSLGIDIRVF-----RTSSLKGVHMLGNLSPRCMCLPKK-----	368
Db	332	VFGSACVVCYSMDVRAFLGLGPLPKHGEPHQWVSGRVPVPRPGMC-PSKTFGTFSST	390
Qy	369	QPIPTETTFQVADSHPEVAQRVEPMG	393
Db	391	KDFPDDVVIQGRNHPLMYNPVLPWG	415

RESULT 5

I48746

semaphorin C - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 03-Nov-2000

C;Accession: I48746

N:R:Puschel, A.W.; Adams, R.H.; Betz, H.  
Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family.

A;Reference number: I48744, MUID:95267431; PMID:7748561

A;Accession: I48746

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-782 <RES>

A;Cross-references: EMBL:X85992; NID:g854327; PIDN:CAAS9984.1; PID:g854328

C;Genetics:

A;Gene: semC

C;Superfamily: semaphorin

[illegible]

RESULT 6  
A49069  
collapsein - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 24-Sep-1999  
C:Accession: A49069  
R:Luo, Y.; Raibite, D.; Raper, J.A.  
Cell 75, 217-227, 1993

A:Title: Collapsin: a protein in brain that induces the collapse and paralysis of new  
A:Reference number: A49069; MUID:94006554; PMID:8402908  
A:Accession: A49069  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-772 <LJ00>  
A:Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079  
C:Superfamily: semaphorin

Query Match	16.5%	Score 350;	DB 2;	Length 772;
Best Local Similarity	28.6%;	Pred. No. 2.8e-21;		
Matches 123; Conservative 56;	Mismatches 165;	Indels 86;	Gaps 19;	

  

Qy	29	LRLRLLLVFWAAASAOQSHRSRSGPRISAVWK----	GODHVPD----	SQEPHTVLFLHEPG	80
Db	7	IALLSLGVLLAGRVNCOHVKNVPRKLKSYKEMLESNNIVFNGLANSSTYFTLLDDEER	66		
Qy	81	SFSVWVGGRGVVYHFNFPFEGKNASRVTVNVI-----	GSTKGSQ-----	DKQDCG	124
Db	67	S-RLYVGAKDHIFSFL-----	VNIKEYKIVMPVSHRSRDECKWAGKDLIRECA	115	
Qy	125	NWITLLR-RCNGLLVCGCTNARKKSCWNL-----	VNDSVMSLGEKGYAPFS	171	
Db	116	NFIKVLKTYNTHLYACGTGAFHPCMTYIEVGSHPEDNIFRMEFS-----	HFENGGRKSPYD	172	
Qy	172	PDENSLVFEQGEVYSTIRKQYENCKIPRRIRIGSELYT----	SDTVMQNPQFIKATIV	228	
Db	173	PKLITASLLVDGELYISGTAADFMRDEFAIFRTLGHHPHPIRTEQHDNRWLNDPRFISAHIL	232		
Qy	229	-HQDAQYDDKTYTYFFREDNPDKNPEAPLNVSRVAQLCRGDGESSLSVSKWNTFLKAML	287		
Db	233	PESONPEDDKLYFFERENALDGEHTGKATHARIGICKNDFGGHSL-VNKWTFLLKARL	291		
Qy	288	VCSDAATN-----RNFNLQDVFLL--	PDPSQGMWRTRVYGVF----	SNPNWYSVAVCVYSLGD	339
Db	292	ICSVPGPNGIDTHEDELQDVFMLNSKDB----	KNPVYGVFTTSNIEFKGSAVCMYSMTD	347	
Qy	340	IDRVF-----	RTSSLKGYHGLNSNPRGMCLPKK-----	QDIPETETQOVADSH	382
Db	348	VRRVFLPGYAHRDGNQYQWVYQGRVYPYPRGTC-PSKTFGGFSDTKDLPDEVITFAKSH	406		
Qy	383	PEVAQRVEPM	392		
Db	407	PAMYNPVFPI	416		

RESULT 7  
I48747  
semaphorin D - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision  
C:Accession: I48747  
R:Puschel, A.W.; Adams, R.H.; Betz, H.  
Neuron 14, 941-948, 1995  
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat  
A:Reference number: I48744; MUID:95267431; PMID:7748561  
A:Accession: I48747  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-772 <RES>  
A:Cross-references: EMBL:X85993; NID:g854329; PID:g854330  
C:Genetics:  
A:Gene: semD  
C:Superfamily: semaphorin

```
Query Match      16.58; Score 349; DB 2; Length 772;
Best Local Similarity 27.94; Pred. No. 3.4e-21;
Matches 117; Conservative 62; Mismatches 165; Indels 76; Gaps 19;
```

Qy 84 VWVGGGRKVVHFNPEPEKNASVTRVNTIGSTKGCQDK-----QDCGNYITLLER-R 133  
 Db 69 LYVAKDHIFESLVNLIKDFQIWPVSYTR---RDECKWAGKDIKCEANFIKVLAYN 125  
 Qy 134 GNCILLVCGTINARKPSCNWL-----VNDSVVMSLGEMKGYAPFSPDENSILVFE 181  
 Db 126 QTHLYACGTGAFHICFYIEVGHHPEDNIFKLODS---HFENGGRKSPYDPKLLTASLLI 182  
 Qy 182 GDEVYSTIRKQEVNGKIPFRFRIRGESELYT---SDTVMQNPQFIKATIV-HODOAYDDK 237  
 Db 183 DGELYSTADEFMCRDFAIFERTICDHUHIPTQEHDSRWLNDPRFISAHLPESDNPEDK 242  
 Qy 238 IYVFFREDNPKNEAPLANVRAQLCRGQGGESSLSVSKWNTFLKAMLVCSDAATN-- 295  
 Db 243 VYFFERNAIGGESHGKATHAIGQICKNDFGGHRSL-VNKWTTFLKARLICSVPGNGI 301  
 Qy 296 -RNFENRLQDVFLL--PDPSCQWRDTRYGVF---SNPWNYSVAVCVYSLGIDIRVF----- 344  
 Db 302 DTHFDELQDVFLLMSKDP---KNPIYGVFTTSSNIFKGSVCMYSMSDVRVFLGPYA 357  
 Qy 345 ----RTSSLGKGYHMLGNRPFGMCLPKK-----OPIPTETFOVADSHPEVAQVRPEM 392  
 Db 358 HRDGNPNQWVPYQGRVPPYPRGTC-PSKTFGGFDSTKDLDDVDITFGRSHPMYNPVPI 416  
 RESULT 8  
 S29921  
 hypothetical protein 15 - vaccinia virus  
 C:Species: vaccinia virus  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 08-Oct-1999  
 C:Accession: S29921  
 R:Amegadzie, B.Y.  
 submitted to the EMBL Data Library, January 1991  
 A:Reference number: S29907  
 A:Accession: S29921  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-441 <AME>  
 A:Cross-references: EMBL:X57318; NID:g62239; PIDN:CAA40587.1; PID:g62254

Query Match 16.1%; Score 341.5; DB 2; Length 441;  
 Best Local Similarity 31.1%; Pred. No. 6.7e-21;  
 Matches 98; Conservative 51; Mismatches 127; Indels 39; Gaps 14;  
 Qy 84 VWVGGGRKVVHFNPEPEKNASVTRVNTIGSTKGCQDKQDCGNYITL---LERRNGLLVC 140  
 Db 74 LYTGVCNAVYTF-----NNKLNT---GLTN-----NNYITTSIKVEDADKDTLVC 117  
 Qy 141 GTNARKPSCNWLNDVSVMSLGEMKGYAPFSPDENSILVFEFGDEVYSTIRKQYNGKIPR 200  
 Db 118 GTNNGNPKCKWIDGSDDPKHG--RGVAPYQNSKVTIISHNGC-VLSDINISKEG--IKR 172  
 Qy 201 FRRIRGES---ELVTSVTMQNPQFIKATIVHQDQAYDDKIYFFREDNPKNEAPLNV 258  
 Db 173 WRRFDGCGYDLYTADNVIPK-DGLRGAFVDKGTY-DKVVILFTDTIGSKR---IVKIP 227  
 Qy 259 RVAQLCRGQGGESSLSVSKWNTFLKAMLVCS-DAATNRNENRLQDVFLLPDPSCGQWRDT 317  
 Db 228 YIAQMLNDEGGSSLSHRSWSTFLKVELECDIDGRSYROI--IHSTIKTD-----NDT 280  
 Qy 318 RVYGVFSNPWNYSVAVCVYSLGIDIRVFTSSLGKGYHMLGNRPFGMCLPKKQPIPTETFQ 377  
 Db 281 ILVVFEDSPYSKALCTYSMTIKQSPSTSKLEGYTKQLPSAPGICLPAGKVVPHHTFE 340  
 Qy 378 VADSHPEVAQVRPEM 392  
 Db 341 VIEKYNVLDIIRKPL 355

RESULT 9  
 E42521  
 A39R protein - vaccinia virus (strain Copenhagen)  
 C:Species: vaccinia virus

A:Note: host Homo sapiens (man)  
 C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 08-Apr-1994  
 C:Accession: E42521  
 R:Johnson, G.P.  
 submitted to GenBank, June 1990  
 A:Reference number: A33172  
 A:Accession: E42521  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-403 <JOH>  
 Query Match 16.1%; Score 340.5; DB 2; Length 403;  
 Best Local Similarity 30.8%; Pred. No. 7.1e-21;  
 Matches 97; Conservative 53; Mismatches 126; Indels 39; Gaps 14;  
 Qy 84 VWVGGGRKVVHFNPEPEKNASVTRVNTIGSTKGCQDKQDCGNYITL---LERRNGLLVC 140  
 Db 36 LYTGVCNAVYTF-----NNKLNT---GLTN-----NNYITTSIKVEDADKDTLVC 79  
 Qy 141 GTNARKPSCNWLNDVSVMSLGEMKGYAPFSPDENSILVFEFGDEVYSTIRKQYNGKIPR 200  
 Db 80 GTNNGNPKCKWIDGSDDPKHG--RGVAPYQNSKVTIISY-NECVLSDINISKEG--IKR 134  
 Qy 201 FRRIRGES---ELVTSVTMQNPQFIKATIVHQDQAYDDKIYFFREDNPKNEAPLNV 258  
 Db 135 WRRFDGCGYDLYTADNVIPK-DGLRGAFVDKGTY-DKVVILFTDTIGSKR---IVKIP 189  
 Qy 259 RVAQLCRGQGGESSLSVSKWNTFLKAMLVCS-DAATNRNENRLQDVFLLPDPSCGQWRDT 317  
 Db 190 YIAQMLNDEGGSSLSHRSWSTFLKVELECDIDGRSYROI--IHSTIKTD-----NDT 242  
 Qy 318 RVYGVFSNPWNYSVAVCVYSLGIDIRVFTSSLGKGYHMLGNRPFGMCLPKKQPIPTETFQ 377  
 Db 243 ILVVFEDSPYSKALCTYSMTIKQSPSTSKLEGYTKQLPSAPGICLPAGKVVPHHTFE 302  
 Qy 378 VADSHPEVAQVRPEM 392  
 Db 303 VIEKYNVLDIIRKPL 317

RESULT 10  
 I48748  
 semaphorin E - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Sep-1999  
 C:Accession: I48748  
 R:Puschel, A.W.; Adams, R.H.; Betz, H.  
 Neuron 14, 941-948, 1995  
 A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat  
 A:Reference number: I48744; MUID:95267431; PMID:7748561  
 A:Accession: I48748  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-751 <RES>  
 A:Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332  
 C:Genetics:  
 A:Gene: seme  
 C:Superfamily: semaphorin  
 Query Match 15.6%; Score 331.5; DB 2; Length 751;  
 Best Local Similarity 26.2%; Pred. No. 9.9e-20;  
 Matches 108; Conservative 68; Mismatches 178; Indels 59; Gaps 16;  
 Qy 33 LLLVFWAAASAGHSRSGPRISAVW-----KQDHVDFS-QPEHTVLFHEPGSFVW 85  
 Db 8 VLVGVFICSTCVRGSQPOQARVYLTDFELRETKTSETFSLSHQOLDYRILLMDQDRIY 67  
 Qy 86 VGGRGKVVHFNPEPEKNAS-----VRTVNIIGSTKGCQD-KQDCGNYITLLER-RG 134  
 Db 68 VGSKDHLISLNI---NNISOEPLSVFVWPASTIKVEECKMAGKDPHTGCGNFVRVIQTFNR 124  
 Qy 135 NGLLVCGTNARKPSCNWL-----VNDSVVM---SLGEMKGYAPFSPDENSILVFEFGDEV 186

Db 125 THLYVCGGAFSPVCTYLNRRSRSDQVFMIDSKCSGKGRCSFNPNVNTSVMIINEELF 184  
QY 187 STIRKQYNGKIPRRIRIRGESELYT---SDTVMQNPQFIKATIVHQ-DQAYDDKITYYFF 242  
Db 185 SGMVIDFMGTDAIFSLTKRQLRTDQHNKWLSEPMFVDAHVIPDGTDPNDKAVYFF 244  
QY 243 REDNPKNPEAPLVNSRVAQLCGDGGESSLSVSKWNTFLKAMLVCS---DAATNRNFN 299  
Db 245 KERLTDNNRSTKQIHSMIARICPNDTGGQORSL-VNKWTFELKARLVCSVTDEGDPETHD 303  
QY 300 RLQDVFLLPDPGQWRDTRVYGVF---SNPNWYSAVCVYSLGDIIDRVFR-----TS 347  
Db 304 ELEDVLELTDNP--RTLLYGIPTSSSVFKGSACVYVHLSIDIQVFNGFPAHKEGPNH 361  
QY 348 SLKGYHMGSLNPRPGMC-----LPKKQPIPTETFEQVADSHPEVAQVPEPM 392  
Db 362 QLISQGRIPYPRPGTCGCAFTPNMRTTKDPDDVVTFIRNHPMYNISPI 414  
RESULT 11  
158169  
semaphorin III - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Sep-1999  
C:Accession: I58169  
R:Wessersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; K  
Neuron 14, 949-959, 1995  
A:Title: Semaphorin III can function as a selective chemorepellent to pattern sensory pr  
A:Reference number: I58169; MUID:95267432; PMID:7748562  
A:Accession: I58169  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-666 <RES>  
A:Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190  
C:Genetics:  
A:Gene: SemalIII  
C:Superfamily: semaphorin  
Query Match 15.5%; Score 329.5; DB 2; Length 666;  
Best Local Similarity 31.3%; Pred. No. 1.2e-19;  
Matches 100; Conservative 42; Mismatches 116; Indels 61; Gaps 14;

QY 121 QDCGNVITLLER-RGNGLLVCGTNAKPCSWNL-----VNDSVVMSLGMKGY 167  
Db 6 KECANFIKVLVAYNQTHLYACGTGAPHPCTVIEVGHHPEDNIFKLODS---HFENGRGK 62  
QY 168 APSPDENSLVLPFGDEVYSTIRKQYNGKIPRRIRIRGESELYT---SDTVMQNPQFIK 224  
Db 63 SPYDPKLLTASLLIDGELYSGTAANPMGRDFAIFRTLGHHHPITRQHDSDRWLNDPRTS 122  
QY 225 ATIV-HQDQAYDDKIYFFREDNPKNPEAPLVNSRVAOLCRDGGESSLSVSKWNTFL 283  
Db 123 AHLIPESDNPEDDKVYFFFRNADGEHSGKATHARIGQICRKNDFGGHRS-L-VNKKWTFEL 181  
QY 284 KAMLVCSDAATN---RNFNLQDVFL--PDPSGQWRDTRVYGVF---SNPNWYSAVCVY 335  
Db 182 KARLICSVPNGIDTHFDELQDVFLMNSKDP----KNPIVYGVFTTSNIFKGSACVY 237  
QY 336 SLGDDIRVFTSSLK-----YHMGSLNPRPGMCLPKK-----QPIPT 373  
Db 238 SMSDVRV-----LLQPYAHRDCPNYQWVPYQGRVYPRPGTC-PSKTFGGFDSTKDLPD 291  
QY 374 ETFQVADSHPEVAQVPEPM 392  
Db 292 DVTIFARSHPAMYNPVFI 310

RESULT 12  
G02173  
semaphorin III family homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 24-Sep-1999  
C:Accession: G02173

R:Naylor, S.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: G09275  
A:Accession: G02173  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-753 <NAV>  
A:Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351  
C:Superfamily: semaphorin  
Query Match 15.4%; Score 327.5; DB 2; Length 753;  
Best Local Similarity 26.4%; Pred. No. 2.2e-19;  
Matches 114; Conservative 63; Mismatches 162; Indels 93; Gaps 19;  
QY 20 SUPAREGLPLRLRLLLVFWVAASAQGH-----SRSGPRISAVWKGDH----- 63  
Db 19 SFTQDHLTPATPKRVLSFKELKATGTAHFNFLLNTDYRI--LLKDEDDHRYVSGKDY 76  
QY 64 --VDFSQPEPHTVLPFHEPGSFSVWVGGRGVYHFNFPPEGKNASVRTVNIIGSTKGCQDK 120  
Db 77 VLSDLHLIDINREPLIIT-----WAASPQRI-----ECCVLSGKDVN----- 112  
QY 121 QDCGNVITLLER-RGNGLLVCGTNAKPCSWNLV-----DSVVM-----SLGEMKGYAP 169  
Db 113 GECGNFVRLIQPNRTHLVYCGGTGAYNPMC-TYVNRGRRAQDYIFYLEPERLESKGKCP 171  
QY 170 FSPDENSLVLPFGDEVYSTIRKQYNGKIPRRIRIRGESELYT---SDTVMQNPQFIKAT 226  
Db 172 YDPKLTASALINEELYAGYIDFMGTAAIFRTLGKQTAMRTDQYNSRWLNDPSTFIAE 231  
QY 227 IVHQDQAYDDKIYFFREDNPKNPEAPLVNSRVAOLCRDGGESSLSVSKWNTFLKAM 286  
Db 232 LIPDSAENDDKLYFFFRERSAEA-POSPAVYARIGRICLINDGCGHCL-VNKKWSTFLKAR 289  
QY 287 LVCS-----DAATNRNFNLQDVFLLPDPGQWRDTR---VYGVFSPNP---WNYSAVCVYSL 337  
Db 290 LVCSVPGEDGIEHFDLQDVFV-----QQTQDVRNPVIYAVFTSSGVSFRGSVAVCYSM 344  
QY 338 GDIDRVFR-----TSSLKGYHMGSLNPRPGMC-----LPKKQPIPTETQVAD 380  
Db 345 ADIRMYFNGFPAHKEGPNYQWVPYSGKMPYPRPGTCGGTFTPTSMKSTKDYDPEVNFMR 404  
QY 381 SHPEVAQVPEPM 392  
Db 405 SHPLMYQAVYPL 416  
RESULT 13  
S66498  
M:sema F protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 24-Nov-1999  
C:Accession: S66498  
R:Inagaki, S.; Furuyama, T.; Iwahashi, Y.  
FEBS Lett. 370, 269-272, 1995  
A:Title: Identification of a member of mouse semaphorin family.  
A:Reference number: S66498; MUID:95385809; PMID:7656991  
A:Accession: S66498  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-834 <INA>  
A:Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599  
C:Superfamily: semaphorin  
F:i-21/Domain: signal sequence #status predicted <SIG>  
F:22-834/Product: M-sema F protein #status predicted <MAT>  
Query Match 14.8%; Score 314; DB 2; Length 834;  
Best Local Similarity 27.8%; Pred. No. 3.5e-18;  
Matches 98; Conservative 50; Mismatches 149; Indels 56; Gaps 12;

QY 84 VWVGRGKVVYHFN-----PEGKNASVRTVNIIGSTKGCQDKQDCGNVITLL 130  
Db 65 LVYVAREALFAFSVEALELQGAISWEAPAEK-----KIECTKGKSNTECFNIRFL 117

Qy 131 E-RRGNGLVCGTNARKSCHNLVNDVSVMSLGM---KGYAPSPDENSILVLFEGDEVY 186  
Db 118 QPNSSHLVCGTYAFQPKCTYINMLTFLDRAEFEDGKGPYPDPKAGHTGLLDGELY 177  
Qy 187 STIRKOEYNGKIPRRIRGESELYSDTV---MONPOFIKATIVHOD---QAYDDKIY 239  
Db 178 SA-TLNNFLGTEPVILRTVGHSHSTKTEYLAFLWNEPHFVGSAFVPSVSGPTGDDDKIY 236  
Qy 240 YFFREDNPKNPEAPLNVSRVAQLCRDGGESSLSVSKWNTFLKAMLVCSDAATNRNFN 299  
Db 237 FFFSERAVEYDCYSQVVARVARKCKDMGARTLQ-KKWTTLKARLVCSAPDKKVVFN 295  
Qy 300 RLQDVFLPDSGQWRDTRVYGVFSNPW---NYSACVYSLGDDIDRVF-----RTS 347  
Db 296 QLKAVHTLGRAS--WHNTTFEGVQARWMDLSACEYQLEIQOVFEGPYKEYSEQAQ 353  
Qy 348 SLKGYHMGSLNPRPGMCL-----PKOPIPTETFOVADSHPEVAORVEP 391  
Db 354 KWARYDVPSPRPGSCINNHNRONGYTSLSLELDPNTLNFITKKHPLMEDQVKP 406  
RESULT 14  
JH0798  
fasciclin IV precursor - American bird grasshopper  
C:Species: Schistocerca americana (American bird grasshopper)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: JH0798  
R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good  
Neuron 9, 831-845, 1992  
A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in  
A:Reference number: JH0798; MUID:93040225; PMID:1418998  
A:Accession: JH0798  
A:Molecule type: mRNA  
A:Residues: 1-730 <KOL>  
A:Cross-references: GB:L00709; NID:g160844; PID:g160845  
A:Experimental source: embryo  
C:Comment: This protein plays a role in growth cone guidance in the developing central n  
C:Keywords: glycoprotein; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-730/Product: fasciclin IV #status predicted <MAT>  
F:23-730/Domain: extracellular #status predicted <EXT>  
F:628-652/Domain: transmembrane #status predicted <TM>  
F:653-730/Domain: intracellular #status predicted <INT>  
F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 14.7%; Score 312; DB 2; Length 730;  
Best Local Similarity 28.9%; Pred. No. 4.2e-18;  
Matches 114; Conservative 57; Mismatches 165; Indels 58; Gaps 19;  
Qy 29 LRLRLLV---FWVAASAQHSRSGPRISAVWKGQHDVD-FSQPEPHTVLFH--EPGSF 82  
Db 1 MRAALVAVALLLWALHAAWVNDVSPKM-VYQFGEERVQRFLGNESHKDFKLEKDNH 59  
Qy 83 SVWVGGRGVYHFNFPPECKNASVTVNIGSI-----KGSQDKQDCGNYITILLER- 132  
Db 60 SLLVGARNIVYNISRLDTEQRIEWHSSGAHRELCYLKGSKD--DCQNYIRVLAKI 117  
Qy 133 RGNGLLVCGTNARKPSCWNLV---NDSVMSLGMKGYAPSPDENSILVLFEGDEVYSTI 189  
Db 118 DDDRVLICGTNAYKPLCRHVALKDGVYVEKEYEGRLCPDPDPHNSTAIYSEGLYSA- 176  
Qy 190 RKQYNGKIPRRIRGESELYSDTVNQ-N-POFIKATIVHODQAYDDKIYFFREDNPD 248  
Db 177 TVADFSGTDPLI--YRGPLRTSRLKQLNAPNFVNT-----MEYNDIFFFFPRETAVE 228  
Qy 249 KNPEAPLNVSRVAQLCRDGGESSLSVSKWNTFLKAMLVCSDAATNR-NFNRLQDVFL- 306  
Db 229 YINGGKAIYSRVARVKHDKGGPHQFG-DRWTSFLKRLNCSVPCDYPFVFNFIQSTSDI 287  
Qy 307 LPDPSGQWRDTRVYGVFSNPWNY---SACVYSLGDI-----DRVFR-----TSS 348  
Db 288 IEGNYGQVEKLIYGVITTPVNSIGGSACVAFSAFSAFSAFSAFSAFSAFSAFSAFSAF 347

Qy 349 LKGYHMGSLNPRPGMCLPKPKKQIPITETFOVADSH 382  
Db 348 LK-----VPEPRPGQCVNDSRRTLPOVSVNFVKSH 376  
RESULT 15  
A49423  
semaphorin I precursor - beetle (Tribolium confusum)  
C:Species: Tribolium confusum  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-May-1999  
C:Accession: A49423  
R:Kolodkin, A.; Matthes, D.J.; Goodman, C.S.  
Cell 75, 1389-1399, 1993  
A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth co  
A:Reference number: A49423; MUID:94094332; PMID:8269517  
A:Accession: A49423  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: mRNA  
A:Residues: 1-711 <KOL>  
A:Cross-references: GB:L26080  
Query Match 14.1%; Score 298; DB 2; Length 711;  
Best Local Similarity 29.4%; Pred. No. 6.2e-17;  
Matches 102; Conservative 55; Mismatches 134; Indels 56; Gaps 18;  
Qy 72 HTVLHFHPCSPFVWVGGRGVYH---FNFPECKNASVTVNIGSI-----TKGSCQDKQD 122  
Db 48 HFIVLNQDET-SILVGGRRNVYVNLISIFDLSEKGRIDWPSSDAHQCLILKGTDD--D 104  
Qy 123 CGNYITLLERRGNG-LLVCGTNARKPSCW---LVNDSVMSLGMKGYAPSPD 173  
Db 105 CONYIRILYSSEPGLKVICGTNSYKPLCRTYAFKRGKYLVEK-----EGIGLCPYNPE 159  
Qy 174 ENSL-VLFEDEVYSTIRKQEVNGKIPRRIRGESELYSDTVNQ-N-POFIKATIVHOD 231  
Db 160 HNSTSVSYNGQLFSATV--ADFSGDPLIYREPORTEL--SDLKOLNAPNFVNSV- 210  
Qy 232 QAYDDKIYFFREDNPKNPEAPLNVSRVAQLCRDGGESSLSVSKWNTFLKAMLVGS- 290  
Db 211 -AYGDYIFFEYRETAVEYMGKGYIYSRVARVKDDKGGPHQ-SRDRWTSFLKARLNCSI 268  
Qy 291 DAATNRNPNRLQDVFLPDPGQWRDTR-VYGVFSNPWNY---SACVYSLGDDIDRVFT 346  
Db 269 PGEPYFFVDEIQSTSDIVEGRYNSDDSKIIYGIILTTPVNAIGGSAICAYOMADILRVFE- 327  
Qy 347 SSLKGYHMGSLN-----PRPGMCLPKKQIPITETFOVADSH 382  
Db 328 GSFKHQETINSNWLVPQNLVPEPRPGQCVNDSRRTLPOVSVNFVKSH 374  
Search completed: March 14, 2003, 09:27:45  
Job time : 16.5226 secs